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OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/028,374

DATE: 01/15/2002
 TIME: 15:24:53

Input Set : A:\ES.txt
 Output Set: N:\CRF3\01152002\J028374.raw

ENTERED

3 <110> APPLICANT: Bristol-Myers Squibb Company
 5 <120> TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN
 EXPRESSED

6 PREDOMINATELY IN BONE MARROW, HLRRBM1
 8 <130> FILE REFERENCE: D0067NP
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/028,374
 C--> 10 <141> CURRENT FILING DATE: 2001-12-20

10 <150> PRIOR APPLICATION NUMBER: US 60/257,773

11 <151> PRIOR FILING DATE: 2000-12-22

13 <160> NUMBER OF SEQ ID NOS: 22

15 <170> SOFTWARE: PatentIn version 3.0

17 <210> SEQ ID NO: 1

18 <211> LENGTH: 4931

19 <212> TYPE: DNA

20 <213> ORGANISM: homo sapiens

22 <220> FEATURE:

23 <221> NAME/KEY: CDS

24 <222> LOCATION: (1320)..(2666)

26 <400> SEQUENCE: 1

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31	tcaggcccgga ggccagcta cgctccccc ggctcccta atcgccattc ggggcttgcg	180
33	ggagcacctg ggaggctcca ccggagcca gacactgcct gccccacgc ccctccagga	240
35	ccctcgaagg agaaggaaat cgggactggc ccagcgtccc gtgctctaga aggcgggcta	300
37	ctgccccgtc ccaagcaggg gaggaggacg agcagggcg tcaactcatc tgtccccgc	360
39	ggaaggatga ggaagctctg ttacctaata tgaaaagctt tctaggagga agtctaagt	420
41	gaacaatgat gcatgaggat gcaatcttac agacacaggg gtctccctat gttgttcaag	480
43	ctggtctoga actcctggcc tcaagtgate ctctgcctc gacctctcaa agctctggta	540
45	ttataggcaa ggagcccagt gataacaaat ggctgtagat gcttttctc catcaagctt	600
47	ccaggaggag atgagatgga gcccatcgct gagccaagaa ttctaatttc atccctttg	660
49	tctttgttca tgctgtgttc tgcttgaat attctccatc ttctttgcct ggaaaagtat	720
51	tacttactga aaccttgaag ccactacctt ctctaaacat tgacaatgca taaccatttg	780
53	ccgagcgttc ttccccggac tgcattcggt tagtctactg agaggcagct cagcgttccc	840
55	aaggagacag atgtctagct ttgtcttttc tgtctgtgtg atgctggaga atcgatatgc	900
57	ccctgggcct ccatctccat ctgtaaaaca agggcatcag ataccccacc tgggtggcccg	960
59	tcctcaattg ggaaccagtc aacatgcctt ctggaagtct ctcttgtcac tccaagaaaa	1020
61	gatccccagg aaacctacag ggactatgtc cgcaggaaat tccggctcat ggaagaccgc	1080
63	aatgcgcgcc taggggaatg tgtcaacctc agccaccggg acaccgggct cctgctggtg	1140
65	aaggagcact caaaccatc gagggtccag cagcagcttc tggacacagg ccggggacac	1200
67	gcgaggaccg tgggacacca ggctagcccc atcaagatag agacctctt tgagccagac	1260
69	gaggagcgcc ccgagccacc gcgcaccgtg gtcatgcaag gcgcggcagg gataggag	1319
71	atg aac cag agt gcc acg gaa tgc agc atg caa gac ctc atc ttc agc	1367
72	Met Asn Gln Ser Ala Thr Glu Cys Ser Met Gln Asp Leu Ile Phe Ser	
73	1 5 10 15	
75	tgc tgg cct gag ccc agc gcg cct ctc cag gag ctc atc cga gtt ccc	1415
76	Cys Trp Pro Glu Pro Ser Ala Pro Leu Gln Glu Leu Ile Arg Val Pro	
77	20 25 30	
79	gag cgc ctc ctt ttc atc atc gac ggc ttc gat gag ctc aag cct tct	1463

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80 Glu Arg Leu Leu Phe Ile Ile Asp Gly Phe Asp Glu Leu Lys Pro Ser
81      35      40      45
83 ttc cac gat cct cag gga ccc tgg tgc ctc tgc tgg gag gag aaa cgg      1511
84 Phe His Asp Pro Gln Gly Pro Trp Cys Leu Cys Trp Glu Glu Lys Arg
85      50      55      60
87 ccc acg gag ctg ctt ctt aac agc tta att cgg aag aag ctg ctc cct      1559
88 Pro Thr Glu Leu Leu Leu Asn Ser Leu Ile Arg Lys Lys Leu Leu Pro
89 65      70      75      80
91 gag cta tct ttg ctc atc acc aca cgg ccc acg gct ttg gag aag ctc      1607
92 Glu Leu Ser Leu Leu Ile Thr Thr Arg Pro Thr Ala Leu Glu Lys Leu
93      85      90      95
95 cac cgt ctg ctg gag cac ccc agg cat gtg gag atc ctg ggc ttc tct      1655
96 His Arg Leu Leu Glu His Pro Arg His Val Glu Ile Leu Gly Phe Ser
97      100      105      110
99 gag gca gaa agg aag gaa tac ttc tac aag tat ttc cac aat gca gag      1703
100 Glu Ala Glu Arg Lys Glu Tyr Phe Tyr Lys Tyr Phe His Asn Ala Glu
101      115      120      125
103 cag gcg ggc caa gtc ttc aat tac gtg agg gac aac gag cct ctc ttc      1751
104 Gln Ala Gly Gln Val Phe Asn Tyr Val Arg Asp Asn Glu Pro Leu Phe
105      130      135      140
107 acc atg tgc ttc gtc ccc ctg gtg tgc tgg gtg gtg tgt acc tgc ctc      1799
108 Thr Met Cys Phe Val Pro Leu Val Cys Trp Val Val Cys Thr Cys Leu
109 145      150      155      160
111 cag cag cag ctg gag ggt ggg ggg ctg ttg aga cag acg tcc agg acc      1847
112 Gln Gln Gln Leu Glu Gly Gly Gly Leu Leu Arg Gln Thr Ser Arg Thr
113      165      170      175
115 acc act gca gtg tac atg ctc tac ctg ctg agt ctg atg caa ccc aag      1895
116 Thr Thr Ala Val Tyr Met Leu Tyr Leu Leu Ser Leu Met Gln Pro Lys
117      180      185      190
119 ccg ggg gcc ccg cgc ctc cag ccc cca ccc aac cag aga ggg ttg tgc      1943
120 Pro Gly Ala Pro Arg Leu Gln Pro Pro Pro Asn Gln Arg Gly Leu Cys
121      195      200      205
123 tcc ttg gcg gca gat ggg ctc tgg aat cag aaa atc cta ttt gag gag      1991
124 Ser Leu Ala Ala Asp Gly Leu Trp Asn Gln Lys Ile Leu Phe Glu Glu
125      210      215      220
127 cag gac ctc cgg aag cac ggc cta gac ggg gaa gac gtc tct gcc ttc      2039
128 Gln Asp Leu Arg Lys His Gly Leu Asp Gly Glu Asp Val Ser Ala Phe
129 225      230      235      240
131 ctc aac atg aac atc ttc cag aag gac atc aac tgt gag agg agc ttc      2087
132 Leu Asn Met Asn Ile Phe Gln Lys Asp Ile Asn Cys Glu Arg Ser Phe
133      245      250      255
135 ctg gca ctc acc agc cgc ttc ctg ttt gga ctc ctg aac gag gag acc      2135
136 Leu Ala Leu Thr Ser Arg Phe Leu Phe Gly Leu Leu Asn Glu Glu Thr
137      260      265      270
139 agg agc cac ctg gag aag agt ctc tgc tgg aag gtc tcg ccg cac atc      2183
140 Arg Ser His Leu Glu Lys Ser Leu Cys Trp Lys Val Ser Pro His Ile
141      275      280      285
143 aag atg gac ctg ttg cag tgg atc caa agc aaa gct cag agc gac ggc      2231
144 Lys Met Asp Leu Leu Gln Trp Ile Gln Ser Lys Ala Gln Ser Asp Gly

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145	290	295	300	
147	tcc acc ctg cag cag ggc tcc ttg gag ttc ttc agc tgc ttg tac gag	2279		
148	Ser Thr Leu Gln Gln Gly Ser Leu Glu Phe Phe Ser Cys Leu Tyr Glu			
149	305	310	315	320
151	atc cag gag gag gag ttt atc cag cag gcc ctg agc cac ttc cag gtg	2327		
152	Ile Gln Glu Glu Glu Phe Ile Gln Gln Ala Leu Ser His Phe Gln Val			
153		325	330	335
155	atc gtg gtc agc aac att gcc tcc aag atg gag cac atg gtc tcc tgc	2375		
156	Ile Val Val Ser Asn Ile Ala Ser Lys Met Glu His Met Val Ser Ser			
157		340	345	350
159	ttc tgt ctg aag cgc tgc agg agc gcc cag gtg ctg cac ttg tat ggc	2423		
160	Phe Cys Leu Lys Arg Cys Arg Ser Ala Gln Val Leu His Leu Tyr Gly			
161		355	360	365
163	gcc acc tac agc gcg gac ggg gaa gac cgc gcg agg tgc tcc gca gga	2471		
164	Ala Thr Tyr Ser Ala Asp Gly Glu Asp Arg Ala Arg Cys Ser Ala Gly			
165		370	375	380
167	gcg cac acg ctg ttg gtg cag cta cca gag agg acc gtt ctg ctg gac	2519		
168	Ala His Thr Leu Leu Val Gln Leu Pro Glu Arg Thr Val Leu Leu Asp			
169	385	390	395	400
171	gcc tac agt gaa cat ctg gca gcg gcc ctg tgc acc aat cca aac ctg	2567		
172	Ala Tyr Ser Glu His Leu Ala Ala Ala Leu Cys Thr Asn Pro Asn Leu			
173		405	410	415
175	ata gag ctg tct ctg tac cga aat gcc ctg ggc agc cgg ggg gtg aag	2615		
176	Ile Glu Leu Ser Leu Tyr Arg Asn Ala Leu Gly Ser Arg Gly Val Lys			
177		420	425	430
179	ctg ctc tgt caa gga ctc aga cac ccc aac tgc aaa ctt cag aac ctg	2663		
180	Leu Leu Cys Gln Gly Leu Arg His Pro Asn Cys Lys Leu Gln Asn Leu			
181		435	440	445
183	agg taaaatttat catatataac atgatatttt gaaataaata tattggccag	2716		
184	Arg			
187	gtagatggc tcacgcctgt aattccagca ctttgggagg cccagatggg gaggatcact	2776		
189	tgacccagga gttcaagacc agcctggcca acatggtgaa accccatctc tactaaaaat	2836		
191	accaaagtga gccaggcatg gtggcacacg tctgtaagcc cagctactca ggaggccaag	2896		
193	gcaggaggat tgcttcaacc caggaggcag aggttgtggc tgaagagggtg ccgcatctcc	2956		
195	agctcagcct gcgaggacct ctctgcagct ctcatagccca ataagaattt gacaaggatg	3016		
197	gatctcagtg gcaacggcgt tggattccca ggcagatgac tgctttgcga gggcctgcgg	3076		
199	catccccaat gcaggctgca gatgattcag ttgaggaagt gtcagctgga gtccggggct	3136		
201	tgtcaggaga tggcttctgt gcttggcacc aaccacatc tggttgagtt ggacctgaca	3196		
203	ggaaatgcac tggaggattt gggcctgagg ttactatgcc agggactgag gcaccagtc	3256		
205	tgcaactac ggactttgtg gctgaagatc tgccgcctca ctgctgctgc ctgtgacgag	3316		
207	ctggcctcaa ctctcagtg gaaccagagc ctgagagagc tggacctgag cctgaatgag	3376		
209	ctgggggacc tgggggtgct gctgctgtgt gagggcctca ggcattccac gtgcaagctc	3436		
211	cagacctgc ggtgagtcct gttttgctca ccaagctagg agtcccaatc catgaacgca	3496		
213	gccctctcac ctgggaccac ggaggccagg ttgtctctgc tcctaaactc tagctactac	3556		
215	atcagccctt tttttttttt ttttgagact cccaagtagc tgagattaca ggcgcccgcc	3616		
217	accaagccca gctaattttt tgtattttta gtagagacag ggtttcatca tgttagcagg	3676		
219	atggtctcga tetactgacc tcatgatctg cctgccttgg cctcccaaag tgctgggatt	3736		
221	acaggcttga gccactgcac ccagcctaca tcagcctttt taaaaggatt tttctggccg	3796		
223	ggcatggttg ctgacacctt aattccagca cttttgggag gccgagggtg gaggatcacc	3856		

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225 tgaggtgggg aattcgagac cagcctgacc aacatgtaga aacaccccat ctgtactaaa 3916
227 aatacaaaag tagccaggca tgggtggtgca tgcctataat gccagctact cgcgaggctg 3976
229 aggaggaga atccgttgaa cccgggaggt ggaagtgtct gtgagctgag atggagccat 4036
231 tgcactccag tctgggcaac aagagcgaaa ctccgtctca aaaaaaaaaa aggggggggt 4096
233 tttctgacgc acggcccttt gcacaagcaa ttcttattcc ctggcatgcc ttctgtcttc 4156
235 tgtccctctt ttgcttgag aagttcaatt tttcttctga acactcttta ctttgtatct 4216
237 tgagacaggg tcttgctctg tcaccagtgc tggagtggag tgggtgtgat atagcccgac 4276
239 atcctgggct gaagccatcc tcccaactca gcctcctgag tagctgggac tgcaagcgca 4336
241 tgccaccaca gatggctaatt ttttactttt tttttgagat tttgccactg cactocagcc 4396
243 tggatgacag agcgagattc catctcaaaa aaaaaaaaga aaaatttcta atttgtgtat 4456
245 atgtgtgtgt ggtggcattc cacaagcata ggagctatgc caactgtatc tcctagtgc 4516
247 tagtataaga cgtgggtaga agtgcataaa aaacacactt tgtgtatttt ttttatcaag 4576
249 gcaccagcaa aaaacaaaaa acaaaaaatc acacacgcgg ctgggcgcgg tggctcatgc 4636
251 ctgtaaacc agcactttgg gaggtgagg cgggtggatc acgaggtcaa gagatggaga 4696
253 ccatcctggc caactggtga aaccccgctt ctactaaaaa tacaaaaatt agctgggcgt 4756
255 ggtggtgtgc acctgtatgc acagctactc aggaggtgga ggcagaagaa tcacttgaac 4816
257 ccaggaggcg gaggttgag tgagccgaga tcgcgccact gcactccagc ctgggcgaca 4876
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262 <210> SEQ ID NO: 2

263 <211> LENGTH: 449

264 <212> TYPE: PRT

265 <213> ORGANISM: homo sapiens

267 <400> SEQUENCE: 2

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274 20 25 30
277 Glu Arg Leu Leu Phe Ile Ile Asp Gly Phe Asp Glu Leu Lys Pro Ser
278 35 40 45
281 Phe His Asp Pro Gln Gly Pro Trp Cys Leu Cys Trp Glu Glu Lys Arg
282 50 55 60
285 Pro Thr Glu Leu Leu Leu Asn Ser Leu Ile Arg Lys Lys Leu Leu Pro
286 65 70 75 80
289 Glu Leu Ser Leu Leu Ile Thr Thr Arg Pro Thr Ala Leu Glu Lys Leu
290 85 90 95
293 His Arg Leu Leu Glu His Pro Arg His Val Glu Ile Leu Gly Phe Ser
294 100 105 110
297 Glu Ala Glu Arg Lys Glu Tyr Phe Tyr Lys Tyr Phe His Asn Ala Glu
298 115 120 125
301 Gln Ala Gly Gln Val Phe Asn Tyr Val Arg Asp Asn Glu Pro Leu Phe
302 130 135 140
305 Thr Met Cys Phe Val Pro Leu Val Cys Trp Val Val Cys Thr Cys Leu
306 145 150 155 160
309 Gln Gln Gln Leu Glu Gly Gly Gly Leu Leu Arg Gln Thr Ser Arg Thr
310 165 170 175
313 Thr Thr Ala Val Tyr Met Leu Tyr Leu Leu Ser Leu Met Gln Pro Lys
314 180 185 190
317 Pro Gly Ala Pro Arg Leu Gln Pro Pro Pro Asn Gln Arg Gly Leu Cys
318 195 200 205

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321 Ser Leu Ala Ala Asp Gly Leu Trp Asn Gln Lys Ile Leu Phe Glu Glu
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325 Gln Asp Leu Arg Lys His Gly Leu Asp Gly Glu Asp Val Ser Ala Phe
326 225                      230                      235                      240
329 Leu Asn Met Asn Ile Phe Gln Lys Asp Ile Asn Cys Glu Arg Ser Phe
330      245                      250                      255
333 Leu Ala Leu Thr Ser Arg Phe Leu Phe Gly Leu Leu Asn Glu Glu Thr
334      260                      265                      270
337 Arg Ser His Leu Glu Lys Ser Leu Cys Trp Lys Val Ser Pro His Ile
338      275                      280                      285
341 Lys Met Asp Leu Leu Gln Trp Ile Gln Ser Lys Ala Gln Ser Asp Gly
342      290                      295                      300
345 Ser Thr Leu Gln Gln Gly Ser Leu Glu Phe Phe Ser Cys Leu Tyr Glu
346 305                      310                      315                      320
349 Ile Gln Glu Glu Glu Phe Ile Gln Gln Ala Leu Ser His Phe Gln Val
350      325                      330                      335
353 Ile Val Val Ser Asn Ile Ala Ser Lys Met Glu His Met Val Ser Ser
354      340                      345                      350
357 Phe Cys Leu Lys Arg Cys Arg Ser Ala Gln Val Leu His Leu Tyr Gly
358      355                      360                      365
361 Ala Thr Tyr Ser Ala Asp Gly Glu Asp Arg Ala Arg Cys Ser Ala Gly
362      370                      375                      380
365 Ala His Thr Leu Leu Val Gln Leu Pro Glu Arg Thr Val Leu Leu Asp
366 385                      390                      395                      400
369 Ala Tyr Ser Glu His Leu Ala Ala Ala Leu Cys Thr Asn Pro Asn Leu
370      405                      410                      415
373 Ile Glu Leu Ser Leu Tyr Arg Asn Ala Leu Gly Ser Arg Gly Val Lys
374      420                      425                      430
377 Leu Leu Cys Gln Gly Leu Arg His Pro Asn Cys Lys Leu Gln Asn Leu
378      435                      440                      445
381 Arg
385 <210> SEQ ID NO: 3
386 <211> LENGTH: 1429
387 <212> TYPE: PRT
388 <213> ORGANISM: homo sapiens
390 <400> SEQUENCE: 3
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396      20                      25                      30
398 His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr
399      35                      40                      45
401 Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln
402      50                      55                      60
404 Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg
405 65                      70                      75                      80
407 Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe
408      85                      90                      95
410 Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date